ABSTRACT:

A Bayesian inference network (BIN) provides an interesting alternative to existing tools for similarity-based virtual screening. The BIN is particularly effective when the active molecules being sought have a high degree of structural homogeneity but has been found to perform less well with structurally heterogeneous sets of actives. In this paper, we introduce an alternative network model, called a Bayesian belief network (BBN), that seeks to overcome this limitation of the BIN approach. Simulated virtual screening experiments with the MDDR, WOMBAT and MUV data sets show that the BIN and BBN methods allow effective screening searches to be carried out. However, the results obtained are not obviously superior to those obtained using a much simpler approach that is based on the use of the Tanimoto coefficient and of the square roots of fragment occurrence frequencies.